

The scores below are sorted by initial score. Significance is calculated based on initial score.

```

X      10      20      30      40      50      60
MDCCEMYWMOGRVCTCCRCRSGOELSKDCGYEGSDACTACPRRYKXSWGHHKCOQSTTC
:      :      :      :      :      :
:      10      20      30      40      50      60
NMGSGPMNYESGSPYNEARNAPADJSLXNGESILMWDIGYAPSVGXLYWTSHERPLLLMYRNRYOREQ
:      :      :      :      :      :
:      10      20      30      40      50      60      70
70      80      90      100      110      120      130
AYINRYOKVNCATSNACGDLRFPRFKRTRIGLDODQDICTKOTPTSEVOCAFOLSLYEADAPVPODE
:      :      :      :      :      :
:      10      20      30      40      50      60      70      80
LGRKANGPRDGLSTGLLAGHNGHERLLCFTISLKTQSTLMSVDELLAVEEERPDGCGKHHXQAAQD
:      :      :      :      :      :
:      10      20      30      40      50      60      70      80      90      100      110      120      130      140

```

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3      -09-695-369A-27 (1-297)
      us-09-840-795-18 sequence 18, Application US/09840795

Initial Score = 17 Optimized Score = 123 Significance = -0.39
Residue Identity = 10% Matches = 32 Mismatches = 241
Gaps = 8 Conservative Substitutions = 15
Translation Frame= 5

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4. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	15	Optimized Score	=	124	Significance	≈	-0.41
Residue Identity	=	10%	Matches	=	31	Mismatches	=	248
Gaps	=	1	Conservative Substitutions	=			=	10
Translation Frame	=	9						

290 X
RLELNVPFEVPS
+
PRHKDMSGAFIASLISGEPDSTFMGLPDM
290 X 300 310

MOQJENEXWQDMGCVCTQRCRGP9G0ELSKDCGYE6GGDADYCTACBPBRYSKSMGHHKCGSCITCAVINRYVK	10	20	30	40	50	60	70
HWXSHECGIMWLPRLQ0SKKCSKSVLVKRTINPLVGDRIICPICRYLALVD							
X	10	20	30	40	50		
VNCSTISMAVCGDCLPFRFKRTRIG--LDQ0ECIPCTKOTPLTSBWQCAPOLSLYEADATPYPGCAETLVML	80	90	100	110	120	130	140
TRQAPAAVAAYE0SPFETTG0GCGCPKRLGT0HWSPWARGREIPLPLFYQPTALNHLHAGVCKRTACSB	60	70	80	90	100	110	120
VSSLIVVYTTLAFILGFLPFLCKOFNRH0RG0GL0GFAADKTAKEBSLEPFPSEKETSAB0QVSENI-PQ0QP	150	160	170	180	190	200	210
GRAPGRGKXTPILG0SVQ0VWMPREGALWYHLEPLPSSTGRHIE0QRKMSACTGCTLGPAGLQ0VSGRTW	130	140	150	160	170	180	190
LNPLLED0CSTSGTPTQ0SFPMASCTSESHSHWYNSPIECHEIDLDQ0FSSSASYTAETLGGNTVYESGDR	220	230	240	250	260	270	280
ANSPR0HXKRLCSAPSEHDXXQHRKXNSDICG0PSC0TCE0GRILCSRHLLHPLHNHPWIAVODHTVGRX	200	210	220	230	240	250	260
290 X							
LELNPFY0PSP							
:							
HTVPLG0STHFLCNPWMBGRKXRTSRMLLENG	280	290	300				

```

6. US-09-695-369A-27 (1.297)
   US-09-840-795-18 Sequence 18, Application US/09640795

Initial Score = 11 Optimized Score = 117 Significance = -0.46
Residue Identity = 7% Matches = 24 Mismatches = 261
Gaps = 12 Conservative Substitutions = 12
Translation Frame= 2

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MDCQENETWQWQKCTYCQRCGPGELEKDCGEGGDATCTACP---PRRTKSWGHHKQCSCTICAVIN
:      :      :      :      :      :      :      :      :      :
ALRWICTGVPEGSKSHLVYRPRSHHGILPRKXVIGPMCTVCCHLPTVWSWTGALQIGIMLRGRCLHSLPSS
X      10      20      30      40      50      60      70
70      80      90      100      110      120      130      140
RVOXVNCATSNVAVCGDCLPRFRKTRIGLQDQDPCIPCTKQPTSEVOCAFQLSLVEDATVPQOATLV
|||      :      :      :      :      :      :      :
OVQXKOLGPPQMSLHHLCCCHQSCSEGLSHYLKCCIMGLFAQVLPKDTWHPRPAQPRVHPVHADPHLXGSMC
80      90      100      110      120      130      140
150      160      170      180      190      200
ALVSSLVVTFLAFLGLFLFYCKQ-----FNNHCQRGGLQFEADKTAKEESLFPVPPSKETSAESQVS
:      :      :      :      :      :      :      :
LPELSSGRCTHSAPSGGHTCCTGEOPAGVYPGILPGLLQAVLQCTLPAMRFAAVXGXNKGISLIP
150      160      170      180      190      200      210
210      220      230      240      250      260      270
ENIFQTOP--LNPFLIEDCSTSGFPTQSFMTMASCSESHSHVHSPLECTELDLQKFSASASYTGAETIG
:      :      :      :      :      :      :
RATQOGDCQXVPSSLGPMQPCPVYLSGLCSYTTTAAAGAXNVMSTRANTLQMGHILSHPTRGILLHFTRTDLE
220      230      240      250      260      270      280
280      290      X
GNTVESTGDRLLELNVPEYVSP
:
HFLPCSLGSOIPHSMWYQTC
290      300      310

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